

TECH CENTER 1600/2900

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/435,733A

DATE: 05/01/2001
 TIME: 18:02:23

Input Set : A:\CIBT-P02-052 SeqList.txt
 Output Set: N:\CRF3\05012001\I435733A.raw

ENTERED

See p. 5

3 <110> APPLICANT: Galdes, Alphonse
 4 Mahanthappa, Nagesh
 6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
 7 PERIPHERAL NEUROPATHIES
 9 <130> FILE REFERENCE: CIBT-P02-052
 11 <140> CURRENT APPLICATION NUMBER: 09/435,733A
 12 <141> CURRENT FILING DATE: 1999-11-08
 14 <160> NUMBER OF SEQ ID NOS: 28
 16 <170> SOFTWARE: PatentIn Ver. 2.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1277
 20 <212> TYPE: DNA
 21 <213> ORGANISM: chicken Shh
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (1)..(1275)
 27 <400> SEQUENCE: 1
 28 atg gtc gaa atg ctg ctg ttg aca aga att ctc ttg gtg ggc ttc atc 48
 29 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
 30 1 5 10 15
 32 tgc gct ctt tta gtc tcc tct ggg ctg act tgt gga cca ggc agg ggc 96
 33 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
 34 20 25 30
 36 att gga aaa agg agg cac ccc aaa aag ctg acc ccg tta gcc tat aag 144
 37 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
 38 35 40 45
 40 cag ttt att ccc aat gtg gca gag aag acc cta ggg gcc agt gga aga 192
 41 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
 42 50 55 60
 44 tat gaa ggg aag atc aca aga aac tcc gag aga ttt aaa gaa cta acc 240
 45 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
 46 65 70 75 80
 48 cca aat tac aac cct gac att att ttt aag gat gaa gag aac acg gga 288
 49 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
 50 85 90 95
 52 gct gac aga ctg atg act cag cgc tgc aag gac aag ctg aat gcc ctg 336
 53 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
 54 100 105 110
 56 gcg atc tcg gtg atg aac cag tgg ccc ggg gtg aag ctg cgg gtg acc 384
 57 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
 58 115 120 125
 60 gag ggc tgg gac gag gat ggc cat cac tcc gag gaa tcg ctg cac tac 432
 61 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
 62 130 135 140
 64 gag ggt cgc gcc gtg gac atc acc acg tcg gat cgg gac cgc agc aag 480
 65 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
 66 145 150 155 160

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68 tac gga atg ctg gcc cgc ctc gcc gtc gag gcc ggc ttc gac tgg gtc 528
69 Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
70 165 170 175
72 tac tac gag tcc aag gcg cac atc cac tgc tcc gtc aaa gca gaa aac 576
73 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
74 180 185 190
76 tca gtg gca gcg aaa tca gga ggc tgc ttc cct ggc tca gcc aca gtg 624
77 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
78 195 200 205
80 cac ctg gag cat gga ggc acc aag ctg gtg aag gac ctg agc cct ggg 672
81 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
82 210 215 220
84 gac cgc gtg ctg gct gct gac gcg gac ggc cgg ctg ctc tac agt gac 720
85 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
86 225 230 235 240
88 ttc ctc acc ttc ctc gac cgg atg gac agc tcc cga aag ctc ttc tac 768
89 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
90 245 250 255
92 gtc atc gag acg cgg cag ccc cgg gcc cgg ctg cta ctg acg gcg gcc 816
93 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Thr Ala Ala
94 260 265 270
96 cac ctg ctc ttt gtg gcc ccc cag cac aac cag tgc gag gcc aca ggg 864
97 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
98 275 280 285
100 tcc acc agt ggc cag gcg ctc ttc gcc agc aac gtg aag cct ggc caa 912
101 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
102 290 295 300
104 cgt gtc tat gtg ctg ggc gag ggc ggc cag cag ctg ctg ccg gcg tct 960
105 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
106 305 310 315 320
108 gtc cac agc gtc tca ttg cgg gag gag gcg tcc gga gcc tac gcc cca 1008
109 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
110 325 330 335
112 ctc acc gcc cag ggc acc atc ctc atc aac cgg gtg ttg gcc tcc tgc 1056
113 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
114 340 345 350
116 tac gcc gtc atc gag gag cac agt tgg gcc cat tgg gcc ttc gca cca 1104
117 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
118 355 360 365
120 ttc cgc ttg gct cag ggc ctg ctg gcc gcc ctc tgc cca gat ggg gcc 1152
121 Phe Arg Leu Ala Gln Gly Leu Ala Ala Leu Cys Pro Asp Gly Ala
122 370 375 380
124 atc cct act gcc gcc acc acc acc act ggc atc cat tgg tac tca cgg 1200
125 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
126 385 390 395 400
128 ctc ctc tac cgc atc ggc agc tgg gtg ctg gat ggt gac gcg ctg cat 1248
129 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
130 405 410 415
132 ccg ctg ggc atg gtg gca ccg gcc agc tg 1277

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133 Pro Leu Gly Met Val Ala Pro Ala Ser
134          420          425
136 <210> SEQ ID NO: 2
137 <211> LENGTH: 1190
138 <212> TYPE: DNA
139 <213> ORGANISM: mouse Dhh
141 <220> FEATURE:
142 <221> NAME/KEY: CDS
143 <222> LOCATION: (1)..(1188)
145 <400> SEQUENCE: 2
146 atg gct ctg ccg gcc agt ctg ttg ccc ctg tgc tgc ttg gca ctc ttg 48
147 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
148 1          5          10          15
150 gca cta tct gcc cag agc tgc ggg ccg ggc cga gga ccg gtt ggc cgg 96
151 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
152 20          25          30
154 cgg cgt tat gtg cgc aag caa ctt gtg cct ctg cta tac aag cag ttt 144
155 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
156 35          40          45
158 gtg ccc agt atg ccc gag cgg acc ctg ggc gcg agt ggg cca gcg gag 192
159 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
160 50          55          60
162 ggg agg gta aca agg ggg tcg gag cgc ttc cgg gac ctc gta ccc aac 240
163 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
164 65          70          75          80
166 tac aac ccc gac ata atc ttc aag gat gag gag aac agc ggc gca gac 288
167 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
168 85          90          95
170 cgc ctg atg aca gag cgt tgc aaa gag cgg gtg aac gct cta gcc atc 336
171 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
172 100          105          110
174 gcg gtg atg aac atg tgg ccc gga gta cgc cta cgt gtg act gaa ggc 384
175 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
176 115          120          125
178 tgg gac gag gac ggc cac cac gca cag gat tca ctc cac tac gaa ggc 432
179 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
180 130          135          140
182 cgt gcc ttg gac atc acc acg tct gac cgt gac cgt aat aag tat ggt 480
183 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
184 145          150          155          160
186 ttg ttg gcg cgc cta gct gtg gaa gcc gga ttc gac tgg gtc tac tac 528
187 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
188 165          170          175
190 gag tcc cgc aac cac atc cac gta tcg gtc aaa gct gat aac tca ctg 576
191 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
192 180          185          190
194 gcg gtc cga gcc gga ggc tgc ttt ccg gga aat gcc acg gtg cgc ttg 624
195 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
196 195          200          205

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198 cgg agc ggc gaa cgg aag ggg ctg agg gaa cta cat cgt ggt gac tgg 672
199 Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
200 210 215 220
202 gta ctg gcc gct gat gca gcg ggc cga gtg gta ccc acg cca gtg ctg 720
203 Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
204 225 230 235 240
206 ctc ttc ctg gac cgg gat ctg cag cgc cgc gcc tcg ttc gtg gct gtg 768
207 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
208 245 250 255
210 gag acc gag cgg cct ccg cgc aaa ctg ttg ctc aca ccc tgg cat ctg 816
211 Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
212 260 265 270
214 gtg ttc gct gct cgc ggg cca gcg cct gct cca ggt gac ttt gca ccg 864
215 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
216 275 280 285
218 gtg ttc gcg cgc cgc tta cgt gct ggc gac tcg gtg ctg gct ccc ggc 912
219 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
220 290 295 300
222 ggg gac gcg ctc cag ccg gcg cgc gta gcc cgc gtg gcg cgc gag gaa 960
223 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
224 305 310 315 320
226 gcc gtg ggc gtg ttc gca ccg ctc act gcg cac ggg acg ctg ctg gtc 1008
227 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
228 325 330 335
230 aac gac gtc ctc gcc tcc tgc tac gcg gtt cta gag agt cac cag tgg 1056
231 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
232 340 345 350
234 gcc cac cgc gcc ttc gcc cct ttg cgg ctg ctg cac gcg ctc ggg gct 1104
235 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
236 355 360 365
238 ctg ctc cct ggg ggt gca gtc cag ccg act ggc atg cat tgg tac tct 1152
239 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
240 370 375 380
242 cgc ctc ctt tac cgc ttg gcc gag gag tta atg ggc/tg 1190
243 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
244 385 390 395
246 <210> SEQ ID NO: 3
247 <211> LENGTH: 1281
248 <212> TYPE: DNA
249 <213> ORGANISM: mouse Ihh
251 <220> FEATURE:
252 <221> NAME/KEY: CDS
253 <222> LOCATION: (1)..(1233)
255 <400> SEQUENCE: 3
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257 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
258 1 5 10 15
260 ctg ctg ctg ctt ctg gtg ccg gcg gcg cgg ggc tgc ggg ccg ggc cgg 96
261 Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg

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262	20	25	30	
264	gtg gtg ggc agc cgc cgg agg ccg cct cgc aag ctc gtg cct ctt gcc	144		
265	Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala			
266	35 40 45			
268	tac aag cag ttc agc ccc aac gtg ccg gag aag acc ctg ggc gcc agc	192		
269	Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser			
270	50 55 60			
272	ggg cgc tac gaa ggc aag atc gcg cgc agc tct gag cgc ttc aaa gag	240		
273	Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu			
274	65 70 75 80			
276	ctc acc ccc aac tac aat ccc gac atc atc ttc aag gac gag gag aac	288		
277	Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn			
278	85 90 95			
280	acg ggt gcc gac cgc ctc atg acc cag cgc tgc aag gac cgt ctg aac	336		
281	Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn			
282	100 105 110			
284	tca ctg gcc atc tct gtc atg aac cag tgg cct ggt gtg aaa ctg cgg	384		
285	Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg			
286	115 120 125			
288	gtg acc gaa ggc cgg gat gaa gat ggc cat cac tca gag gag tct tta	432		
289	Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu			
290	130 135 140			
292	cac tat gag ggc cgc gcg gtg gat atc acc acc tca gac cgt gac cga	480		
293	His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg			
294	145 150 155 160			
296	aat aag tat gga ctg ctg gcg cgc tta gca gtg gag gcc ggc ttc gac	528		
297	Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp			
298	165 170 175			
300	tgg gtg tat tac gag tcc aag gcc cac gtg cat tgc tct gtc aag tct	576		
301	Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser			
302	180 185 190			
304	gag cat tcg gcc gct gcc aag aca ggt ggc tgc ttt cct gcc gga gcc	624		
305	Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala			
306	195 200 205			
308	cag gtg cgc cta gag aac ggg gag cgt gtg gcc ctg tca gct gta aag	672		
309	Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys			
310	210 215 220			
312	cca gga gac cgg gtg ctg gcc atg ggg gag gat ggg acc ccc acc ttc	720		
313	Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe			
314	225 230 235 240			
316	agt gat gtg ctt att ttc ctg gac cgc gag cca aac cgg ctg aga gct	768		
317	Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala			
318	245 250 255			
320	ttc cag gtc atc gag act cag gat cct ccg cgt cgg ctg gcg ctc acg	816		
321	Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr			
322	260 265 270			
324	cct gcc cac ctg ctc ttc att gcg gac aat cat aca gaa cca gca gcc	864		
325	Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala			
326	275 280 285			

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 05/01/2001

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Input Set : A:\CIBT-P02-052 SeqList.txt

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L:728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1613 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15
L:1613 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:1613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2192 M:283 W: Missing Blank Line separator, <220> field identifier
L:2239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2539 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2542 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22